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SEQUENCE LISTING

<110> Gurney, Mark E.

Li, Jinhe

Pauley, Adele M.

Pharmacia & Upjohn Company

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Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

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Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

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Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

        115                 120                 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

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Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145                 150                 155                 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

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Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

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Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

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Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

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Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

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Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

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Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

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Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg

420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro

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Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp

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Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr

485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn

500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile

515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln

530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser

545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe

565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580 585 590

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35 40 45

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg

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Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser

65 70 75 80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp

85 90 95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser

100 105 110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser

115 120 125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser

130 135 140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln

145 150 155 160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr

165 170 175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr

180 185 190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu

195 200 205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg

210 215 220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr

225 230 235 240

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys

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Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu

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Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly

                325                 330                 335

Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met

            340                 345                 350

His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu

        355                 360                 365

Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly

    370                 375                 380

His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val

385                 390                 395                 400

Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu

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Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu

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Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile

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Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly

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His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val

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Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly

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Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val

500 505 510

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp

515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn

530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile

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Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln
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Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu
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Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu
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Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro

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Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu

145                 150                 155                 160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile

                165                 170                 175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe

            180                 185                 190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp

        195                 200                 205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly

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Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr

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Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr

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Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val

305 310 315 320

Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr

325 330 335

Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys

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Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met

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Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln

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Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val

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Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr

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Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln

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Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys

465                 470                 475                 480

Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp

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Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly

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Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly

35 40 45

Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr

50 55 60

Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln

65 70 75 80

Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp

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Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro

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Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu

115 120 125

Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln

130 135 140

Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg

145 150 155 160

Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg

165 170 175

Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala

180 185 190

Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu

195 200 205

Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys

210 215 220

Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr

225 230 235 240

Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val

245 250 255

Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile

260 265 270

Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr

275 280 285

Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys

290 295 300

Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr

305 310 315 320

Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met

325 330 335

Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val

340 345 350

Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr

355 360 365

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser

370 375 380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser

385 390 395 400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr

405 410 415

Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu

420 425 430

Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr

435 440 445

Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala

450 455 460

Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp

465 470 475 480

Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg

485 490 495

Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg

500 505 510

Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn

515 520 525

Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met

530 535 540

Lys

545

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro

65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp

100 105 110

```
Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe

        115                 120                 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

    130                 135                 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu

145                 150                 155                 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

                165                 170                 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His

            180                 185                 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val

        195                 200                 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly

    210                 215                 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser

225                 230                 235                 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly

                245                 250                 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
```

```
        260                 265                 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
    275                 280                 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu
    290                 295                 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp
305                 310                 315                 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
                325                 330                 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr
            340                 345                 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
        355                 360                 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
    370                 375                 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385                 390                 395                 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
                405                 410                 415
```

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala

420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln

435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln

450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys

465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu

485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn

500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr

515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

530 535 540

<210> 8

<211> 589

<212> PRT

<213> Homo sapiens

<400> 8

```
Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val
1               5                   10                  15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys
            20                  25                  30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg
        35                  40                  45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser
    50                  55                  60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly
65                  70                  75                  80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala
                85                  90                  95

Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro
            100                 105                 110

Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly
        115                 120                 125

Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro
    130                 135                 140
```

```
Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg
145                 150                 155                 160

Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser
                165                 170                 175

Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr
            180                 185                 190

Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys
        195                 200                 205

Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile
    210                 215                 220

Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln
225                 230                 235                 240

His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys
                245                 250                 255

Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys
            260                 265                 270

Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp
        275                 280                 285
```

```
Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly

    290                 295                 300

Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser

305                 310                 315                 320

Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile

                325                 330                 335

His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His

            340                 345                 350

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp

        355                 360                 365

Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala

    370                 375                 380

Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala

385                 390                 395                 400

Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu

                405                 410                 415

His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp

            420                 425                 430

Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp

        435                 440                 445
```

```
Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser

    450                 455                 460

Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn

465                 470                 475                 480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu

                485                 490                 495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu

            500                 505                 510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val

        515                 520                 525

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr

    530                 535                 540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser

545                 550                 555                 560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu

                565                 570                 575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

            580                 585
```

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys

1 5 10 15

Arg Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser

20 25 30

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr

35 40 45

Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu

50 55 60

Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val

65 70 75 80

Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp

85 90 95

Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys

100 105 110

Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe

```
        115                 120                 125

Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val

    130                 135                 140

Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys

145                 150                 155                 160

Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys

                165                 170                 175

Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys

            180                 185                 190

Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile

        195                 200                 205

Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser

    210                 215                 220

Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln

225                 230                 235                 240

Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys

                245                 250                 255

Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His

            260                 265                 270
```

```
Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser

        275                 280                 285

Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu

    290                 295                 300

Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His

305                 310                 315                 320

Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg

                325                 330                 335

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His

            340                 345                 350

Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser

        355                 360                 365

Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr

    370                 375                 380

Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln

385                 390                 395                 400

Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg

                405                 410                 415

Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His
```

420 425 430

Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser

435 440 445

Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln

450 455 460

Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr

465 470 475 480

Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly

485 490 495

Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu

500 505 510

Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg

515 520 525

Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr

530 535 540

Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

545 550 555

<210> 10

<211> 540

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro

65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp

100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe

115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu

145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His

180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val

195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly

210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser

225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly

245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr

260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His

275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu

290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp

305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala

325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr

340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His

355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly

370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp

385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu

405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala

420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln

435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln

450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys

465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu

485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn

500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr

515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

530 535 540

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 11

cgggatccac catggatgat ggatcgatga cacc 34

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 12

ggaattcctt aagggtatac agcatcaaag tcg 33

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 13

tcacttcatg tccacatcaa agtcc 25

```
<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:

      Oligonucleotide primer


<400> 14

ggtaattaca agttcttgtt gaactg                                      26


<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:

      Oligonucleotide primer


<400> 15

ccctgcaacg tgtgtagaca gg                                          22


<210> 16

<211> 24

<212> DNA
```

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 16

ccagtctctg cattccacac tttg 24

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 17

ctcagacagg tcaggacatt tgg 23

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 18

ggaattccat gaaaagattg gaccatggtt ctg 33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 19

ggaattcctc acttcatgtc acatcaaagt ccag 34

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged
homo sapiens

<400> 20

atggagcaaa agctcatttc tgaagaggac ttgaatgaaa tggagcaaaa gctcatttct 60

gaagaggact tgaatgaaat ggagcaaaag ctcatttctg aagaggactt gaatgaaatg 120 gagcaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaagct catttctgaa 180

gaggacttga atgaaatgga gagcttgggc gacctcacca tggagcaaaa gctcatttct 240

gaagaggact tgaattccat gaaaagaaag ttggaccatg gttctgaggt ccgctctttt 300

tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtacca 360

tgttcagcaa caccaacaac ttttggggac ctcagagcag ccaatggcca agggcaacaa 420

cgacgccgaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480

cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540

ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600

tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcctggaacc caaagacctg 660

ctacaagcag ctcagacatg tcgctactgg agaattttgg ctgaagacaa ccttctctgg 720

agagagaaat gcaaagaaga ggggattgat gaaccattgc acatcaagag aagaaaagta 780

ataaaaccag gtttcataca cagtccatgg aaaagtgcat acatcagaca gcacagaatt 840

gatactaact ggaggcgagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900

catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtggttc tgatgacaac 960

actttaaaag tttggtcagc agtcacaggc aaatgtctga gaacattagt gggacataca 1020

ggtggagtat ggtcatcaca aatgagggac aacatcatca ttagtggatc tacagatcgg 1080

acactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140

tccactgtgc gttgtatgca tcttcatgaa aaaagagttg ttagcggttc tcgagatgcc 1200

actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggtcatgtt 1260

gcagcagtcc gctgtgttca atatgatggc aggagggttg ttagtggagc atatgatttt 1320

atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380

aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440

tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500

tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560

acagttaaaa tctgggatat caaaacagga cagtgtttac aaacattgca aggtcccaac 1620

aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680

gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740

acattggaga gtgggggggag tgggggagtt gtgtggcgga tcagagcctc aaacacaaag 1800

ctggtgtgtg cagttgggag tcggaatggg actgaagaaa ccaagctgct ggtgctggac 1860 tttgatgtgg acatgaagtg a 1881

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged
homo sapien

<400> 21

```
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln
  1               5                  10                  15

Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile
             20                  25                  30

Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu
         35                  40                  45

Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
     50                  55                  60

Glu Met Glu Ser Leu Gly Asp Leu Thr Met Glu Gln Lys Leu Ile Ser
 65                  70                  75                  80

Glu Glu Asp Leu Asn Ser Met Lys Arg Lys Leu Asp His Gly Ser Glu
```

85 90 95

Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr

100 105 110

Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe

115 120 125

Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile

130 135 140

Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe

145 150 155 160

Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile

165 170 175

Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu

180 185 190

Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala

195 200 205

Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala

210 215 220

Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp

225 230 235 240

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys

245 250 255

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser

260 265 270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu

275 280 285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr

290 295 300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn

305 310 315 320

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu

325 330 335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile

340 345 350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu

355 360 365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg

370 375 380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala

385 390 395 400

Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu

405 410 415

Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg

420 425 430

Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu

435 440 445

Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr

450 455 460

Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr

465 470 475 480

Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu

485 490 495

Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile

500 505 510

Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys

515 520 525

Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser

530 535 540

```
Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser
545                 550                 555                 560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile
                565                 570                 575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp
            580                 585                 590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg
        595                 600                 605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp
    610                 615                 620

Met Lys
625



<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence


<220>

<223> Description of Artificial Sequence:

      Oligonucleotide primer
```

<400> 22

gggtacccct cattattccc tcgagttctt c 31

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc 29

<210> 24

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged
homo sapien

<400> 24

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60

ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120

tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaag cagccggaca 180

cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240

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ttaaaaatga tttttacaa aatgaaaaga aagttggacc atggttctga ggtccgctct 300

ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360

ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420

caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480

tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540

gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600

atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660

ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720

tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780

gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840

attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900

gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960

aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020

acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080

cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140

acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200

gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260

gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320

tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380

actaatagag tctattcatt acagtttgat ggtatccatg tggtgagtgg atctcttgat 1440

acatcaatcc gtgtttggga tgtggagaca gggaattgca ttcacacgtt aacagggcac 1500

cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560

tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaaacatt gcaaggtccc 1620

aacaagcatc agagtgctgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680

tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740

gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800

aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860

gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
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tctagagggc ccttcgaagg taagcctatc cctaaccctc tcctcggtct cgattctacg 1980

cgtaccggtc atcatcacca tcaccattga 2010

<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged
homo sapien

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225 230 235 240

```
Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

                245                 250                 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

            260                 265                 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

        275                 280                 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

    290                 295                 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305                 310                 315                 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

                325                 330                 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

            340                 345                 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

        355                 360                 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

    370                 375                 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
```

385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg

420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro

435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp

465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr

485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn

500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile

515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln

530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser

545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe

565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu

625 630 635 640

Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His

660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
homo sapiens

<400> 26

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60

ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120

tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaag cagccggaca 180

cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240

ttaaaaatga ttttttacaa aatgaaaaga aagttggacc atggttctga ggtccgctct 300

ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360

ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420

caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480

tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540

gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600

atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660

ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720

tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780

gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840

attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900

gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960

aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020

acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080

cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140

acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200

gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320

tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380

actaatagag tctattcatt acagtttgat ggtatccatg tggtgagtgg atctcttgat 1440

acatcaatcc gtgtttggga tgtggagaca gggaattgca ttcacacgtt aacagggcac 1500

cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560

tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaaacatt gcaaggtccc 1620

aacaagcatc agagtgctgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680

tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740

gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800

aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860

gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920

tctagagggc ccttcgaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980

catcatcacc atcaccattg a 2001

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165 170 175

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Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

            180                 185                 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

        195                 200                 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

    210                 215                 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225                 230                 235                 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

                245                 250                 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

            260                 265                 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

        275                 280                 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

    290                 295                 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305                 310                 315                 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

                325                 330                 335
```

```
Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
            340                 345                     350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
        355                 360                 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
    370                 375                 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
385                 390                 395                 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
                405                 410                 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
            420                 425                 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
        435                 440                 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
    450                 455                 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465                 470                 475                 480
```

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr

485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn

500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile

515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln

530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser

545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe

565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu

625 630 635 640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

645 650 655

Met His Thr Gly His His His His His His

660 665

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 28

tcacttcatgtccacatcaaagtcc 25

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

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<400> 29
ggtaattacaaagttcttgttgaactg                                    27

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer

<400> 30
ccctgcaacgtgtgtagacagg                                         22

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primer

<400> 31
ccagtctctgcattccacactttg                                              24

<210> 32
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 32

ctcagacaggtcaggacatttgg 23